

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Ammons, William Steve et al.
- (ii) TITLE OF INVENTION: Method of Treating Conditions Associated with Intestinal Ischemia/Reperfusion
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: United States of America
  - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY INFORMATION:
  - (A) NAME: Sharp, Jeffrey S.
  - (B) REGISTRATION NUMBER: 31,879
  - (C) REFERENCE/DOCKET NUMBER: 27129/32043
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 312/474-6300
  - (B) TELEFAX: 312/474-0448
  - (C) TELEX: 25-3856

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1813 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 31..1491
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 124..1491

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(D) OTHER INFORMATION: "rBPI"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC	54
Met Arg Glu Asn Met Ala Arg Gly	
-31 -30 -25	
CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA	102
Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile	
-20 -15 -10	
GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC	150
Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
-5 1 5	
TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG	198
Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu	
10 15 20 25	
CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT	246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
30 35 40	
AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC	534
Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
155 160 165	
ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG	678
Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys	
170 175 180 185	
CTG CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA ATA GAT TCT	726

Leu	Gln	Pro	Tyr	Phe	Gln	Thr	Leu	Pro	Val	Met	Thr	Lys	Ile	Asp	Ser	
				190					195					200		
GTG	GCT	GGA	ATC	AAC	TAT	GGT	CTG	GTG	GCA	CCT	CCA	GCA	ACC	ACG	GCT	774
Val	Ala	Gly	Ile	Asn	Tyr	Gly	Leu	Val	Ala	Pro	Pro	Ala	Thr	Thr	Ala	
			205					210					215			
GAG	ACC	CTG	GAT	GTA	CAG	ATG	AAG	GGG	GAG	TTT	TAC	AGT	GAG	AAC	CAC	822
Glu	Thr	Leu	Asp	Val	Gln	Met	Lys	Gly	Glu	Phe	Tyr	Ser	Glu	Asn	His	
		220					225					230				
CAC	AAT	CCA	CCT	CCC	TTT	GCT	CCA	CCA	GTG	ATG	GAG	TTT	CCC	GCT	GCC	870
His	Asn	Pro	Pro	Pro	Phe	Ala	Pro	Pro	Val	Met	Glu	Phe	Pro	Ala	Ala	
	235					240					245					
CAT	GAC	CGC	ATG	GTA	TAC	CTG	GGC	CTC	TCA	GAC	TAC	TTC	TTC	AAC	ACA	918
His	Asp	Arg	Met	Val	Tyr	Leu	Gly	Leu	Ser	Asp	Tyr	Phe	Phe	Asn	Thr	
	250				255					260					265	
GCC	GGG	CTT	GTA	TAC	CAA	GAG	GCT	GGG	GTC	TTG	AAG	ATG	ACC	CTT	AGA	966
Ala	Gly	Leu	Val	Tyr	Gln	Glu	Ala	Gly	Val	Leu	Lys	Met	Thr	Leu	Arg	
			270					275						280		
GAT	GAC	ATG	ATT	CCA	AAG	GAG	TCC	AAA	TTT	CGA	CTG	ACA	ACC	AAG	TTC	1014
Asp	Asp	Met	Ile	Pro	Lys	Glu	Ser	Lys	Phe	Arg	Leu	Thr	Thr	Lys	Phe	
			285					290					295			
TTT	GGA	ACC	TTC	CTA	CCT	GAG	GTG	GCC	AAG	AAG	TTT	CCC	AAC	ATG	AAG	1062
Phe	Gly	Thr	Phe	Leu	Pro	Glu	Val	Ala	Lys	Lys	Phe	Pro	Asn	Met	Lys	
		300					305					310				
ATA	CAG	ATC	CAT	GTC	TCA	GCC	TCC	ACC	CCG	CCA	CAC	CTG	TCT	GTG	CAG	1110
Ile	Gln	Ile	His	Val	Ser	Ala	Ser	Thr	Pro	Pro	His	Leu	Ser	Val	Gln	
	315					320					325					
CCC	ACC	GGC	CTT	ACC	TTC	TAC	CCT	GCC	GTG	GAT	GTC	CAG	GCC	TTT	GCC	1158
Pro	Thr	Gly	Leu	Thr	Phe	Tyr	Pro	Ala	Val	Asp	Val	Gln	Ala	Phe	Ala	
	330				335				340					345		
GTC	CTC	CCC	AAC	TCC	TCC	CTG	GCT	TCC	CTC	TTC	CTG	ATT	GGC	ATG	CAC	1206
Val	Leu	Pro	Asn	Ser	Ser	Leu	Ala	Ser	Leu	Phe	Leu	Ile	Gly	Met	His	
			350					355					360			
ACA	ACT	GGT	TCC	ATG	GAG	GTC	AGC	GCC	GAG	TCC	AAC	AGG	CTT	GTT	GGA	1254
Thr	Thr	Gly	Ser	Met	Glu	Val	Ser	Glu	Glu	Ser	Asn	Arg	Leu	Val	Gly	
			365					370					375			
GAG	CTC	AAG	CTG	GAT	AGG	CTG	CTC	CTG	GAA	CTG	AAG	CAC	TCA	AAT	ATT	1302
Glu	Leu	Lys	Leu	Asp	Arg	Leu	Leu	Leu	Glu	Leu	Lys	His	Ser	Asn	Ile	
		380					385					390				
GGC	CCC	TTC	CCG	GTT	GAA	TTG	CTG	CAG	GAT	ATC	ATG	AAC	TAC	ATT	GTA	1350
Gly	Pro	Phe	Pro	Val	Glu	Leu	Leu	Gln	Asp	Ile	Met	Asn	Tyr	Ile	Val	
	395				400					405						
CCC	ATT	CTT	GTG	CTG	CCC	AGG	GTT	AAC	GAG	AAA	CTA	CAG	AAA	GGC	TTC	1398
Pro	Ile	Leu	Val	Leu	Pro	Arg	Val	Asn	Glu	Lys	Leu	Gln	Lys	Gly	Phe	
	410				415				420					425		
CCT	CTC	CCG	ACG	CCG	GCC	AGA	GTC	CAG	CTC	TAC	AAC	GTA	GTG	CTT	CAG	1446
Pro	Leu	Pro	Thr	Pro	Ala	Arg	Val	Gln	Leu	Tyr	Asn	Val	Val	Leu	Gln	
				430				435					440			
CCT	CAC	CAG	AAC	TTC	CTG	CTG	TTC	GGT	GCA	GAC	GTT	GTC	TAT	AAA		1491
Pro	His	Gln	Asn	Phe	Leu	Leu	Phe	Gly	Ala	Asp	Val	Val	Tyr	Lys		

445	450	455	
TGAAGGCACC	AGGGGTGCCG	GGGGCTGTCA	GCCGCACCTG TTCCTGATGG GCTGTGGGGC 1551
ACCGGCTGCC	TTTCCCCAGG	GAATCCTCTC	CAGATCTTAA CCAAGAGCCC CTTGCAAAC 1611
TCTTCGACTC	AGATTCAGAA	ATGATCTAAA	CACGAGGAAA CATTATTCAT TGGAAAAGTG 1671
CATGGTGTGT	ATTTTAGGGA	TTATGAGCTT	CTTTCAAGGG CTAAGGCTGC AGAGATATTT 1731
CCTCCAGGAA	TCGTGTTTCA	ATTGTAACCA	AGAAATTTC ATTTGTGCTT CATGAAAAAA 1791
AACTTCTGGT	TTTTTTCATG	TG	1813

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Glu	Asn	Met	Ala	Arg	Gly	Pro	Cys	Asn	Ala	Pro	Arg	Trp	Val	-31	-30	-25	-20
Ser	Leu	Met	Val	Leu	Val	Ala	Ile	Gly	Thr	Ala	Val	Thr	Ala	Ala	Val	-15	-10	-5	1
Asn	Pro	Gly	Val	Val	Val	Arg	Ile	Ser	Gln	Lys	Gly	Leu	Asp	Tyr	Ala	5	10	15	
Ser	Gln	Gln	Gly	Thr	Ala	Ala	Leu	Gln	Lys	Glu	Leu	Lys	Arg	Ile	Lys	20	25	30	
Ile	Pro	Asp	Tyr	Ser	Asp	Ser	Phe	Lys	Ile	Lys	His	Leu	Gly	Lys	Gly	35	40	45	
His	Tyr	Ser	Phe	Tyr	Ser	Met	Asp	Ile	Arg	Glu	Phe	Gln	Leu	Pro	Ser	50	55	60	65
Ser	Gln	Ile	Ser	Met	Val	Pro	Asn	Val	Gly	Leu	Lys	Phe	Ser	Ile	Ser	70	75	80	
Asn	Ala	Asn	Ile	Lys	Ile	Ser	Gly	Lys	Trp	Lys	Ala	Gln	Lys	Arg	Phe	85	90	95	
Leu	Lys	Met	Ser	Gly	Asn	Phe	Asp	Leu	Ser	Ile	Glu	Gly	Met	Ser	Ile	100	105	110	
Ser	Ala	Asp	Leu	Lys	Leu	Gly	Ser	Asn	Pro	Thr	Ser	Gly	Lys	Pro	Thr	115	120	125	
Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	His	Ile	Asn	Ser	Val	His	Val	His	130	135	140	145
Ile	S	r	Lys	Ser	Lys	Val	Gly	Trp	Leu	Ile	Gln	Leu	Phe	His	Lys	150	155	160	
Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	165	170	175	

[illegible]